

#6



PCT10

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/030,271

DATE: 08/21/2002
TIME: 15:44:48

Input Set : A:\217860US.ST25.txt
Output Set: N:\CRF4\08212002\J030271.raw

3 <110> APPLICANT: OTA, TOSHIO
 4 ISOGAI, TAKAO
 5 NISHIKAWA, TETSUO
 6 HIO, YURI
 7 MIYOSHI, SOUSUKE
 8 SATOH, SUSUMU
 10 <120> TITLE OF INVENTION: APOPTOSIS-ASSOCIATED FACTOR
 12 <130> FILE REFERENCE: 217860US0PCT
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/030,271
 C--> 15 <141> CURRENT FILING DATE: 2002-06-28
 17 <150> PRIOR APPLICATION NUMBER: JP 11-194179
 18 <151> PRIOR FILING DATE: 1999-07-08
 20 <150> PRIOR APPLICATION NUMBER: US 60/159,586
 21 <151> PRIOR FILING DATE: 1999-10-18
 23 <160> NUMBER OF SEQ ID NOS: 13
 25 <170> SOFTWARE: PatentIn version 3.1
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 909
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Homo sapiens
 32 <220> FEATURE:
 33 <221> NAME/KEY: CDS
 34 <222> LOCATION: (1)..(909)
 35 <223> OTHER INFORMATION:
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 43 tgc ctg gac tac tac ggg atg ctg tcg ctt cac cgt atg ttc gag gtg 96
 44 Cys Leu Asp Tyr Tyr Gly Met Leu Ser Leu His Arg Met Phe Glu Val
 45 20 25 30
 47 gtg ggc ggg caa ctg acc gag tgc gag ctg gag ctc ctg gcc ttt ctg 144
 48 Val Gly Gly Gln Leu Thr Glu Cys Glu Leu Glu Leu Ala Phe Leu
 49 35 40 45
 51 ctg gat gag gct cct ggc gcc gga ggc tta gcc cgg gcc cgc agc 192
 52 Leu Asp Glu Ala Pro Gly Ala Ala Gly Gly Leu Ala Arg Ala Arg Ser
 53 50 55 60
 55 ggc cta gag ctc ctg gag ctg gag cgc cgc ggg cag tgc ggc gag 240
 56 Gly Leu Glu Leu Leu Glu Leu Glu Arg Arg Gly Gln Cys Gly Glu
 57 65 70 75 80
 59 agc aac ctg cgg ctg ctg ggg caa ctc ctg cgc gtg ctg gcc cgc cac 288
 60 Ser Asn Leu Arg Leu Leu Gly Gln Leu Leu Arg Val Leu Ala Arg His
 61 85 90 95

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64	Asp	Leu	Leu	Pro	His	Leu	Ala	Arg	Lys	Arg	Arg	Arg	Arg	Pro	Val	Ser	Pro		
65						100			105							110			
67	gaa	cgc	tat	agc	tat	ggc	acc	tcc	agc	tct	tca	aag	agg	aca	gag	ggt		384	
68	Glu	Arg	Tyr	Ser	Tyr	Gly	Thr	Ser	Ser	Ser	Ser	Lys	Arg	Thr	Glu	Gly			
69						115			120							125			
71	agc	tgc	cgt	cgc	cgt	cg	cag	tca	agc	agt	tct	gca	aat	tct	cag	cag		432	
72	Ser	Cys	Arg	Arg	Arg	Arg	Gln	Ser	Ser	Ser	Ser	Ala	Asn	Ser	Gln	Gln			
73						130			135			140							
75	ggt	cag	tgg	gag	aca	ggc	tcc	ccc	cca	acc	aag	cg	cag	cg	cg	agt		480	
76	Gly	Gln	Trp	Glu	Thr	Gly	Ser	Pro	Pro	Thr	Lys	Arg	Gln	Arg	Arg	Ser			
77	145					150				155						160			
79	cgg	ggc	cgg	ccc	agt	ggt	gcc	aga	cg	cg	cg	aga	ggg	gcc	cca		528		
80	Arg	Gly	Arg	Pro	Ser	Gly	Gly	Ala	Arg	Arg	Arg	Arg	Arg	Gly	Ala	Pro			
81						165			170			175							
83	gcc	gca	ccc	cag	cag	cag	tca	gag	ccc	gcc	aga	cct	tcc	tct	gaa	ggc		576	
84	Ala	Ala	Pro	Gln	Gln	Ser	Glu	Pro	Ala	Arg	Pro	Ser	Ser	Glu	Gly				
85						180			185			190							
87	aaa	gtg	acc	tgt	gac	atc	cg	ctc	cg	gtt	cg	gca	gag	tac	tgc	gag		624	
88	Lys	Val	Thr	Cys	Asp	Ile	Arg	Leu	Arg	Val	Arg	Ala	Glu	Tyr	Cys	Glu			
89						195			200			205							
91	cat	ggg	cca	gcc	ttg	gag	cag	ggc	gtg	gca	tcc	cg	cg	ccc	cag	g		672	
92	His	Gly	Pro	Ala	Leu	Glu	Gln	Gly	Val	Ala	Ser	Arg	Arg	Pro	Gln	Ala			
93						210			215			220							
95	ctg	g	cg	cag	ctg	gac	gtg	ttt	gg	cag	ggc	acc	gca	gtg	ctg	cg		720	
96	Leu	Ala	Arg	Gln	Leu	Asp	Val	Phe	Gly	Gln	Ala	Thr	Ala	Val	Leu	Arg			
97	225					230				235						240			
99	tca	agg	gac	ctg	ggc	tct	gtg	gtt	tgt	gac	atc	aag	ttc	tca	gag	ctc		768	
100	Ser	Arg	Asp	Leu	Gly	Ser	Val	Val	Cys	Asp	Ile	Lys	Phe	Ser	Glu	Leu			
101						245			250			255							
103	tcc	tat	ctg	gac	gcc	ttc	tgg	ggc	gac	tac	ctg	agt	ggc	gcc	ctg	ctg		816	
104	Ser	Tyr	Leu	Asp	Ala	Phe	Trp	Gly	Asp	Tyr	Leu	Ser	Gly	Ala	Leu	Leu			
105						260			265			270							
107	cag	gcc	ctg	cg	ggc	gtg	ttc	ctg	act	gag	ggc	ctg	cga	gag	gct	gtg		864	
108	Gln	Ala	Leu	Arg	Gly	Val	Phe	Leu	Thr	Glu	Ala	Leu	Arg	Glu	Ala	Val			
109						275			280			285							
111	ggc	cg	gag	gct	gtt	cg	ctg	gt	act	gag	ggc	ctg	cga	gag	gct	g		909	
112	Gly	Arg	Glu	Ala	Val	Arg	Leu	Leu	Val	Ser	Val	Asp	Glu	Ala	Asp				
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127	Cys	Leu	Asp	Tyr	Tyr	Gly	Met	Leu	Ser	Leu	His	Arg	Met	Phe	Glu	Val			
128						20			25			30							
131	Val	Gly	Gly	Gln	Leu	Thr	Glu	Cys	Glu	Leu	Glu	Leu	Leu	Ala	Phe	Leu			

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135	Leu Asp Glu Ala Pro Gly Ala Ala Gly Gly Leu Ala Arg Ala Arg Ser			
136	50	55	60	
139	Gly Leu Glu Leu Leu Leu Glu Leu Glu Arg Arg Gly Gln Cys Gly Glu			
140	65	70	75	80
143	Ser Asn Leu Arg Leu Leu Gly Gln Leu Leu Arg Val Leu Ala Arg His			
144	85	90	95	
147	Asp Leu Leu Pro His Leu Ala Arg Lys Arg Arg Arg Pro Val Ser Pro			
148	100	105	110	
151	Glu Arg Tyr Ser Tyr Gly Thr Ser Ser Ser Ser Lys Arg Thr Glu Gly			
152	115	120	125	
155	Ser Cys Arg Arg Arg Gln Ser Ser Ser Ser Ala Asn Ser Gln Gln			
156	130	135	140	
159	Gly Gln Trp Glu Thr Gly Ser Pro Pro Thr Lys Arg Gln Arg Arg Ser			
160	145	150	155	160
163	Arg Gly Arg Pro Ser Gly Gly Ala Arg Arg Arg Arg Arg Gly Ala Pro			
164	165	170	175	
167	Ala Ala Pro Gln Gln Ser Glu Pro Ala Arg Pro Ser Ser Glu Gly			
168	180	185	190	
171	Lys Val Thr Cys Asp Ile Arg Leu Arg Val Arg Ala Glu Tyr Cys Glu			
172	195	200	205	
175	His Gly Pro Ala Leu Glu Gln Gly Val Ala Ser Arg Arg Pro Gln Ala			
176	210	215	220	
179	Leu Ala Arg Gln Leu Asp Val Phe Gly Gln Ala Thr Ala Val Leu Arg			
180	225	230	235	240
183	Ser Arg Asp Leu Gly Ser Val Val Cys Asp Ile Lys Phe Ser Glu Leu			
184	245	250	255	
187	Ser Tyr Leu Asp Ala Phe Trp Gly Asp Tyr Leu Ser Gly Ala Leu Leu			
188	260	265	270	
191	Gln Ala Leu Arg Gly Val Phe Leu Thr Glu Ala Leu Arg Glu Ala Val			
192	275	280	285	
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213	aggagtcatc ggacgccaga atctggccgg gttctgagct tggccgcct ccctcccccg	120		
215	gga atg gcg cta tcc ggg tcg acc ccg gcc ccg tgc tgg gag gag gat	168		
216	Met Ala Leu Ser Gly Ser Thr Pro Ala Pro Cys Trp Glu Glu Asp			
217	1 5 10 15			
219	gag tgc ctg gac tac tac ggg atg ctg tcg ctt cac cgt atg ttc gag	216		
220	Glu Cys Leu Asp Tyr Tyr Gly Met Leu Ser Leu His Arg Met Phe Glu			

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224	Val	Val	Gly	Gly
225	35	40	45	
227	ctg	ctg	gat	gag
228	Leu	Leu	Asp	Glu
229	50	55	60	
231	agc	ggc	cta	gag
232	Ser	Gly	Leu	Glu
233	65	70	75	
235	gag	agc	aac	ctg
236	Glu	Ser	Asn	Leu
237	80	85	90	95
239	cac	gac	ctg	ctg
240	His	Asp	Leu	Leu
241	100	105	110	
243	cca	gaa	cgc	tat
244	Pro	Glu	Arg	Tyr
245	115	120	125	
247	ggt	agt	tgc	cgt
248	Gly	Ser	Cys	Arg
249	130	135	140	
251	cag	ggt	cag	tgg
252	Gln	Gly	Gln	Trp
253	145	150	155	
255	agt	cgg	ggc	ccc
256	Ser	Arg	Gly	Arg
257	160	165	170	175
259	cca	gcc	gca	ccc
260	Pro	Ala	Ala	Pro
261	180	185	190	
263	ggc	aaa	gtg	acc
264	Gly	Lys	Val	Thr
265	195	200	205	
267	gag	cat	ggg	cca
268	Glu	His	Gly	Pro
269	210	215	220	
271	gcg	ctg	gcg	cag
272	Ala	Leu	Ala	Arg
273	225	230	235	
275	cgc	tca	agg	gac
276	Arg	Ser	Arg	Asp
277	240	245	250	255
279	ctc	tcc	tat	ctg
280	Leu	Ser	Tyr	Leu
281	260	265	270	
283	ctg	cag	gcc	ctg
284	Leu	Gln	Ala	Leu
285	275	280	285	

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291	tat	gag	gct	ggc	cgg	cgc	cgc	ctg	ttg	ctg	atg	gag	gag	gaa	ggg	ggg	1080
292	Tyr	Glu	Ala	Gly	Arg	Arg	Arg	Leu	Leu	Leu	Met	Glu	Glu	Glu	Gly	Gly	
293	305					310						315					
295	cgg	cgc	ccg	aca	gag	gcc	tcc	tgatccagga	ctggcaggat	tgatcccacc							1131
296	Arg	Arg	Pro	Thr	Glu	Ala	Ser										
297	320					325											
299	tccaaagtctc	cggggccacct	tctccctggga	ggacgaccat	ctctaccct	tgacagcccc											1191
301	tcccacagga	tgtgggctct	gaggcctaaa	ccatttccag	ctgagttcc	ttcccgagact											1251
303	cctcttaccc	ccagggtgtc	ccccttagcc	tccggaggcg	ggggctggc	ctgtatctca											1311
305	gaaggggaggg	gcacagctac	acactcacca	aaggcccccc	tgcacattgt	atctctgatc											1371
307	ttgggctgtc	tgcactgtca	caggtgcaca	cactcgctca	tgctcacact	gcccctgctg											1431
309	agatcttccc	tgggcctctg	ccctggcctg	cttcccagca	cacacttctt	tggcctaagg											1491
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313	ggcactggag	ctggggtgca	catggggcct	gctcaccttg	cccacacatc	tccagccagc											1611
315	cagggccctg	cccagcttca	attacagac	ctgactctcc	tcaccttccc	ccctgctgtc											1671
317	cagagctgaa	catagacttg	cacttggatg	tcacctggag	tgtcacatgg	gagtgttatg											1731
319	gcagcatcat	accaaggcct	actgttgac	atggggccaa	aaccagtaaa	cagccacctt											1791
321	cttggaaagg	aatgcaaag	gctttggggg	tgatggaaaa	gacctttac	aaatgatacc											1851
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338					20				25				30				
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345	Leu	Asp	Glu	Ala	Pro	Gly	Ala	Ala	Gly	Gly	Leu	Ala	Arg	Ala	Arg	Ser	
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353	Ser	Asn	Leu	Arg	Leu	Leu	Gly	Gln	Leu	Leu	Arg	Val	Leu	Ala	Arg	His	
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357	Asp	Leu	Leu	Pro	His	Leu	Ala	Arg	Lys	Arg	Arg	Arg	Pro	Val	Ser	Pro	
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365	Ser	Cys	Arg	Arg	Arg	Arg	Gln	Ser	Ser	Ser	Ser	Ala	Asn	Ser	Gln	Gln	
366							130				135			140			
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370							145				150			155			160
373	Arg	Gly	Arg	Pro	Ser	Gly	Gly	Ala	Arg	Arg	Arg	Arg	Arg	Gly	Ala	Pro	
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VERIFICATION SUMMARY

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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date